

GenCore version 4.5  
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## OM nucleic - nucleic search, using sw model

Run on: March 2, 2002, 20:03:30 : Search time 1496.56 Seconds  
(without alignments)  
2929.570 Million cell updates/sec

Title: US-09-540-235-1  
Perfect score: 408  
Sequence: 1 accgcgcgtatgagaatta.....acatccatcaatgttgtta 408

Scoring table: IDENTITY\_NUC  
Gapop 10.0 , Gapept 1.0

Searched: 11351937 segs, 5372889281 residues

Total number of hits satisfying chosen parameters: 22703874

Minimum DB seq length: 0  
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

## Database :

EST:\*  
1: em\_estfun:\*  
2: em\_esthum:\*  
3: em\_estin:\*  
4: em\_estom:\*  
5: em\_estpl:\*  
6: em\_estda:\*  
7: em\_estro:\*  
8: em\_estov:\*  
9: em\_hic:\*  
10: gb\_est1:\*  
11: gb\_est2:\*  
12: gb\_hic:\*  
13: gb\_gss:\*  
14: em\_gss\_fun:\*  
15: em\_gss\_hum:\*  
16: em\_gss\_inv:\*  
17: em\_gss\_pln:\*  
18: em\_gss\_pro:\*  
19: em\_gss\_rod:\*  
20: em\_gss\_vrt:\*  
21: em\_gss\_other:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length DB	ID	Description
1	133.8	32.8	454	10	BE636128 SNEST4a15
2	133.8	32.8	489	10	AL381742 MTRC02F09
3	133.2	32.6	637	13	AQ963432 LERGL927R
4	131.6	32.3	649	13	AQ963431 LERGL927R
5	130.4	32.0	409	11	BF052600 EST437830
6	130.4	32.0	487	11	BE924162 EST437830
7	130.4	32.0	612	11	BI178667 EST519612
8	129	31.6	340	10	BI164427 A061P34U
9	129	31.6	467	11	BF517187 NXSL_011
10	128.8	31.6	477	10	AI164301 A058P78u
11	128.4	31.5	471	10	AW289566 NXNV00260
12	127.6	31.3	389	10	AL388757 MTRC50E10

13	127	31.1	349	10	AA841097	AA841097 MB3D6A3E
14	126.4	31.0	525	10	A1490797	A1490797 EST241505
15	126.4	31.0	527	10	A1772648	A1772648 EST253748
16	126.4	31.0	534	10	A1490076	A1490076 EST248415
17	126.4	31.0	538	10	AM040995	AM040995 EST283859
18	126.4	31.0	564	10	BE450458	BE450458 EST401345
19	126.4	31.0	566	11	BG133272	BG133272 EST465164
20	126.4	31.0	595	11	A1482959	A1482959 EST242282
21	126.4	31.0	609	11	BG123744	BG123744 EST469390
22	126.4	31.0	625	10	AM220037	AM220037 EST302520
23	126.4	31.0	744	11	BG123632	BG123632 EST469278
24	126	30.9	396	11	BG627962	BG627962 CC-est1c1
25	126	30.9	439	11	BG643800	BG643800 EST511994
26	126	30.9	477	10	AM037370	AM037370 EST275908
27	126	30.9	489	10	A1778920	A1778920 EST259799
28	126	30.9	535	10	A1775702	A1775702 EST256802
29	126	30.9	560	11	BG134065	BG134065 EST466957
30	126	30.9	601	11	B1210092	B1210092 EST528132
31	126	30.9	604	11	B1209065	B1209065 EST527105
32	126	30.9	621	11	BG127514	BG127514 EST473256
33	126	30.9	627	11	BG130661	BG130661 EST476288
34	126	30.9	648	11	BG129875	BG129875 EST475521
35	125.4	30.7	379	10	AM290853	AM290853 NKV047G1
36	125.2	30.7	401	11	BF610389	BF610389 NXSL_058-
37	124.8	30.6	531	10	A1484130	A1484130 EST248881
38	124.6	30.5	553	11	B1179552	B1179552 EST520497
39	124.6	30.5	607	10	AM906936	AM906936 EST343059
40	124.6	30.5	615	11	BG598740	BG598740 EST503640
41	124.6	30.5	616	11	BG600593	BG600593 EST505488
42	124.6	30.5	629	11	BG598622	BG598622 EST503522
43	124.2	30.4	543	11	BG817601	BG817601 ESU0023
44	123.2	30.2	441	10	A1778533	A1778533 EST259412
45	122.8	30.1	667	11	BF707483	BF707483 9A5 CDNA

## ALIGNMENTS

RESULT 1  
BE636128 454 bp mRNA EST 25-AUG-2000  
LOCUS SNEST4a15f07.y1 csn 1 s neurona invitro metozoite CDNA Sarcocystis  
DEFINITION neurona CDNA 5' similar to FR:082579 082579 RIBOSOMAL PROTEIN L26  
; mRNA sequence.

ACCESSION BE636128 GI:9918815  
VERSION BE636128.1  
KEYWORDS Sarcocystis neurona.  
SOURCE Sarcocystis neurona.  
ORGANISM Sarcocystis neurona.  
Eukaryota; Alveolata; Apicomplexa; Coccidia; Eimeriida;  
Sarcocystidae; Sarcocystis.

REFERENCE 1 (bases 1 to 454)  
Howe,D.K., Stamper,S., Tang,K., Sibley,L.D., Clifton,S., Marra,M.,  
Hiller,L., Pape,D., Martin,J., Wylie,T., Theisling,B., Bowers,Y.,  
Gibbons,M., Rilter,E., McCann,R., Bilstain,A., Benne,J., Schmitt,  
A., Ronko,I., Tsagarelisvilli,R., Fedele,M., Belaygorod,L.,  
Franklin,C., Carr,L.M., Grow,A., Maguire,L., Wadkins,J., Richey,J.,  
Waterston,R. and Wilson,R.

TITLE Sarcocystis neurona EST project  
JOURNAL Unpublished (2000)  
COMMENT Contact: Daniel K. Howe  
Sarcocystis neurona EST project  
Washington University School of Medicine  
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA  
Tel: 314 286 1800  
Fax: 314 286 1810  
Email: est@watson.wustl.edu  
Contact Daniel K. Howe (dkhowe2@pop.uky.edu) for further  
information relating to organism, libraries, or clone availability.  
Seq primer: 40RP from Gibco  
High quality sequence stop: 401.  
Location/Qualifiers  
1. 454

FEATURES  
source

Contact : Pascal Gamas and Etienne-Pascal Journet, Laboratoire de Biologie Moléculaire des Relations Plantes-Microorganismes, CNRS-INRA, BP 27 31326 Castanet-Tolosan Cedex, France (Email : [Mt-est@toulouse.inra.fr](mailto:Mt-est@toulouse.inra.fr) Website : <http://sequence.toulouse.inra.fr/Mtruncacula.html>).

FEATURES  
source

```

/organism="Sarcocystis neurona"
/strain="Sn3"
/db_xref="taxon:42890"
/clone.lib="cSn_1_S_neurona_invitto_merozoite_cDNA"
/dev_stage="merozoite"
/lab_host="DH10B"
/notes="Vector: pBluescript SK-; Site_1: EcoRI; Site_2:
XhoI; The library was constructed by Dan Howe, University
of Kentucky. cDNAs were synthesized from poly(A)+ RNA
by oligo d(T) priming and directionally cloned into the
Uni-ZAP XR lambda vector. The library was mass excised
as phageids and rescued in SOCR cells. The plasmid
library was recovered from the SOCR cells and transformed
in mass into DH10B cells for sequencing. WARNING: the
library contains a small percentage of cDNAs derived from
the bovine host cells."

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BASE COUNT	125 a	105 c	137 g	87 t
ORIGIN				

Query Match	32.8%;	Score 133.8;	DB 10;	Length 454;
Best Local Similarity	64.2%;	Pred. No. 2e-27;		
Matches 201;	Conservative	0;	Mismatches 112;	Indels 0;
				Gaps 0;

OY	96	atgaaatattccaaagtgtgatctgctgtctagaagaagaagaaagaaagatattccaa	155
Db	134	ATGAAGTTCAAGTTACCGCGTACGTCGTCCGAAGGAAGCGCGCAAGCCGCACTTACC	193
OY	156	gcacacattcttctagcaagaaatccatgagtgacccttctcagaagaactacgtacg	215
Db	194	GCCCGCTGGAACGTGCACAGGAAATTTATGCGGCACCTCTTTGCAAGGAATCTCGCAG	253
OY	216	aaatcacagcgtctgtcttaccattccgaagaagaagaagatcatagtttcgcgga	275
Db	254	AAGTCAACAGTCCGCTGCTGCCATCATAGGAATAATATGAAGTGAATGATGTCGGGA	313
OY	276	gcttcaagagtagagaagaagaagtaccagctgltatcgaagaataatcgtatatac	335
Db	314	CATACACACGCCGCCGAGGGAAGAGTGTGAAAGTTTACAGGAAGAGTGGTTATCCAT	373
OY	336	atcgagagatgtaaccagagaanaagcgaaatggaaatgacttacctgtggtgaatacatca	395
Db	374	ATTGAGAGAGTTTACCACAGACGAACAGGACAGGAAAGTCAGTGCATTCGGGATTCA	433
OY	396	tctaagtgtgta	408
Db	434	AGCAAGTTGTCA	446

/note="Vector: plhuscript psk, site.1: EcoRI; Site.2: XhoI; M. truncatula sterilised seeds were germinated for 72h at 25 C, before transplanting into a 1/3 Eponises soll root fragments colonized by the abubscular mycorrhizal fungus Glomus intraradices (Schenck & Smith, isolate LP8 ). The plants were watered every day and twice a week with a modified nutrient long Ashton solution without phosphate but with a high level of nitrate. After 3 weeks RNA was extracted from whole root systems. cDNA was prepared from polyA+ enriched RNA. The cDNA was directionally ligated into Uni-zap XR vector from Stratagene and packaged using Gispack Gold packaging extracts. Plasmids containing cDNA inserts were mass-excised from phage stocks using Exasit helper phage and propagated in SOLR cells. Clone ordering and sequencing was performed by the Centre National de Sequençage (Genoscope, Evry, France). Note : EST may be of fungal origin."

BASE COUNT	186 a	71 c	100 g	132 t
ORIGIN				

Query Match	32.8%;	Score 133.8;	DB 10;	Length 489;
Best Local Similarity	64.28;	Pred. No. 2e-27;		
Matches 201; Conservative	0;	Mismatches 112;	Indels 0;	Gaps 0

OY	94	ccatgaagatltccaagtgtatcgcgtctagaaagaacagaggaaagcattcttc	153
Db	4	CAATGAATTCCTTAAAGATGTTAGTTCCTCCACGCTAAAGCCGAAAGCCCATTTT	63
OY	154	aagcacatctctgtacgaagaaatactatgagtgacacctgtccaagaaactaagta	213
Db	64	CTGCTCCTCTTGCGTGGCGGAGAAATTAAGATGTCGATTATCCAAAGAACTTGAAG	123
OY	214	cgaaatacagcttgcgttcttcttactacttcgaaagaagacgaatataatagtcgcg	273
Db	124	ACCAATTAATAATACTCGCATCTATTACCAATTCTGTAAGATGATGAAAGTTGATCGTACGTG	183
OY	274	gagcttcaagggtagaagaagaaagtltaacaagtglttalcgaagaagaaatalcgaatc	333
Db	184	GTACTTTAAAGGTCGTGATCGAAGAAAGTACAGGTTTATCCAGACAGATGGGTTATCC	243
OY	334	atatcgagagagtgaccagagaaaacggaatggatgatctgtacctgtgyggaataatc	393
Db	244	AAATTGATCGCATCGTAGAGAAATAAAGCGGTAACTGTTCCAGTTGGATTATCATC	303
OY	394	catctaatgttgt 406	
Db	304	CATCAAAATGTTGT 316	

RESULT	2
LOCUS	AL381742
DEFINITION	AL381742 489 bp mRNA EST 03-AUG-2000
ACCESSION	MTBC02F09f3
VERSION	MTBC02F09f3
KEYWORDS	sequence.
ORGANISM	AL381742
SOURCE	AL381742.1 GI:9681493
REFERENCE	EST.
AUTHORS	barrel medic.
TITLE	Medicago truncatula
JOURNAL	Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
COMMENT	Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
	Rosidae; eurosids I; Fabales; Fabaceae; Papilionoideae; Trifoliaceae
	Medicago.
	1 (bases 1 to 489)
	Journet,E.P., Crespeau,H., van Tuinen,D., Gouzy,J., Tallon,O.,
	Nlebel,A., Carreau,V., Chataigner,O., Kahn,D., Gianinazzi-Pearson
	,V. and Gamas,P.
	Medicago truncatula ESTs from endomycorrhizal roots
	Unpublished (2000)
	Contact: Genoscope
	Genoscope of Centre National de Sequencage
	Bp 191 91006 EVRY cedex - France
	Email: sequefr@genoscope.cns.fr, Web : www.genoscope.cns.fr

[illegible]

KEYWORDS	GSS.
SOURCE	thale cress.
ORGANISM	Arabidopsis thaliana Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae; eurosids II; Brassicales; Brassicaceae; Arabidopsis. 1 (bases 1 to 637)
REFERENCE	Buell, C. R., Lin, X., Pal, G., Barnstead, M., Bowman, C., Ullrich, T., Feldguy, T., Liang, F., Creasy, T. and Fraser, C. M. Genomic survey sequencing of Landsberg erecta ecotype of Arabidopsis thaliana and identification of sequence-based polymorphisms
TITLE	Unpublished (2000)
JOURNAL	Contact: Xiaoying Lin The Institute for Genomic Research 9712 Medical Center Dr., Rockville, MD 20850, USA Tel: 301 838 0200 Fax: 301 838 0208 Email: atet@igr.org
COMMENT	For additional information, see <a href="http://www.tigr.org/tdb/at/at.html">http://www.tigr.org/tdb/at/at.html</a> Seq primer: TR Class: shotgun.

BASE COUNT	208 a	144 c	131 g	154 t	
ORIGIN					
Query Match			32.6%	Score 133.2;	DB 13; Length 637;
Best Local Similarity			63.4%	Pred. No. 3.1e-27;	
Matches 204; Conservative			0;	Mismatches 118;	Indels 0; Gaps 0;
Qy	87	tcagtcgcacatgaatattccaaagtgtatcgttctgtcttaagaagaacagagaagca	146		
Db	312	tcggcgggcgatmaattcattccgcgctgtgaccttcttcgccgggaamaacaggaagcct	371		
Qy	147	tacttcaagaccacactctctctgtacgaagaatcacatgagtgaccccttgcgaagaa	206		
Db	372	cacttcacagacgtcccttcaagccttagcgccgcttctcattagagctgcgccttattccaaagac	431		
Qy	207	ctaagtcagaaataacagcgttgcgttcttacctattctgaagaagaagaagaatcatca	266		
Db	432	ctcccttaacaaataacaaagctgacattccattgcgcgatttcttaagaacagcgaagtgcaatt	491		
Qy	267	gttcgcggaagcttcaagaggtctagaagaagaagaattacaacgttgtattcgaaagaatat	326		
Db	492	gtttcctggagcgttcmaaggaaagaaaggaaggagtcagtgatccgccgcgaatgcg	551		
Qy	337	cgaatataatcgaagaagtgaccagagaagaagaacgaattggaatgactgttaccggtgga	386		
Db	552	gtgatgtcacattcgaagagaaatcacaaaggagaaagtcaacgaaccacaggttaacctcga	611		
Qy	387	ataacatcatctaatgttgtta	408		
Db	612	gtcaatgcttgcgaatgtgatga	633		

RESULT	4		
AO963431/c			
LOCUS			
DEFINITION	AO963431	649 bp	DNA
	LERGL92TF	LERG	Arabidopsis thaliana genomic clone LERGL92, DNA
	sequence.		
ACCESSION	AO963431		
VERSION	AO963431.1	GI:6791132	
KEYWORDS	GSS.		
SOURCE	thale cress.		

ORGANISM	REFERENCE	AUTHORS	TITLE	JOURNAL	COMMENT
Arbidopsis thaliana					
Eukaryota: Viridiplantae: Streptophyta; Embryophyta; Tracheophyta;					
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;					
Rosidae; eustosids II: Brassicales; Brassicaceae; Arabidopsis.					
1 (bases 1 to 649)					
Buell, C. R., Lin, X., Pai, G., Barnstead, M., Bowman, C., Ullrichbach, T.,					
Feldblum, T., Liang, F., Greasy, T. and Fraser, C. M.					
Genomic survey sequencing of Landsberg erecta ecotype of					
Arbidopsis thaliana and identification of sequence-based					
polymorphisms					
Unpublished (2000)					
Contact: Xiaoying Lin					
The Institute for Genomic Research					
9712 Medical Center Dr., Rockville, MD 20850, USA					
Tel.: 301 838 0200					
Fax: 301 838 0208					
Email: atc@tigr.org					
For additional information, see <a href="http://www.tigr.org/tdb/at/at.html">http://www.tigr.org/tdb/at/at.html</a>					
Seq primer: TF					
Class: shotgun.					

BASE COUNT	156 a	143 c	149 g	201 t	ORIGIN
Query Match	32.3%;	Score 131.6;	DB 13;	Length 649;	/note="Organ: Leaf; Vector: pUD19K; Total genomic DNA was
Best Local Similarity	63.0%;	Pred. No. 8.7e-27;			sheared to 0.4-0.7 kbp before ligation."
Matches 203;	Conservative 0;	Mismatches 119;	Indels 0;	Gaps 0;	
QY	87	tcagtcgcacgaagatctccaagattgcttcgtctctagaaagaacagagaaagca	146		
Db	383	TCGGGGGGGATGAAGTTCATCCCGGTGACCTTTCTCCCGGAGAACAGAGAGCT	324		
QY	147	tacttcaagacacatctctctgacagaaactacatgagtgtgaacctgtccaagaa	206		
Db	323	CACCTTCACAGCTCCTTCACAGCGTAGGGCGCTTCTCATGACTCGCCGTTATCCAAGAC	264		
QY	207	ctacgtacgaatacaagcgcttcgtctcttacctatctcgaaagaagaagaaatcata	266		
Db	263	CTCCGTAAACAATATCAACGCTCAGATCCATGCCGATTCTGTAAGAAGACAGAGTAGTGCAGTT	204		
QY	267	gttcgcgagcttccaaggttagagaaagaaagtctacaagtgcttatacgaaagaatat	326		
Db	203	GTTTGCTGGGACCTTCAAGGAGAAAGGAGAGGTGATGACAGGTCTATCCGCCCAAGTGG	144		
QY	327	cgaatcacatctcgaagagtgaccagagaataaagcgaatgaaatgactgtacctgtgga	386		
Db	143	GTGATTCACATCGAGAGATCAACAAGGAGAAAGTTCACAGCAACCCGCGTCAAGCTCGA	84		
QY	387	atacatccatctaattgttgtta	408		
Db	83	GTCAATGCTTCGAATGTGATGA	62		

RESULT	5
LOCUS	BF052600
DEFINITION	BF052600 409 bp mRNA
ACCESSION	EST47880 potato leaves and petioles Solanum tuberosum cDNA clone
VERSION	CS882.F20 5' sequence, mRNA sequence.
KEYWORDS	BF052600.1 GI:10806496
SOURCE	EST.
ORGANISM	Potato.
	Solanum tuberosum
	Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta

## REFERENCE

Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Asteridae; euasterids I; Solanales; Solanaceae; Solanum. 1 (bases 1 to 409)  
van der Hoeven, R.S., Bezzerides, J., Holt, I.E., Liang, F., Cho, J., Utterback, T., Hansen, C.L., Doan, B., Bougri, O., Buell, C.R., Ronning, C.M., Fry, W.E., Tanksley, S.D. and Baker, B.  
Generation of ESTs from potato leaves and petioles  
Unpublished (2000)

## TITLE

Journal  
Contact: Cathy Ronning  
The Institute for Genomic Research  
For clone info: please contact Research Genetics, Libraries  
Division tel 1-800-711-6195, email cdna@esgen.com.

## COMMENT

## FEATURES

source  
Location/Qualifiers  
1. 409  
/organism="Solanum tuberosum"  
/cultivar="Kennebec"  
/db\_xref="taxon:4113"  
/clone="GSTB32E20"  
/clone\_1lb="potato leaves and petioles"  
/tissue\_type="leaflets and petioles"  
/dev\_stage="8 weeks old plants"  
/lab\_host="SOLR"  
/note="Vector: pBluescript SK(-); Site\_1: EcoRI; Site\_2: XhoI. Tissue was supplied by Dr. Fry (Cornell University). Leaflets and petioles were isolated from 8 week old greenhouse grown plants. The plants were watered and fertilized freely. The tissue was immediately frozen in liquid nitrogen."  
BASE COUNT 120 a 81 c 103 g 105 t  
ORIGIN

Query Match 32.0%; Score 130.4; DB 11; Length 409;  
Best Local Similarity 62.7%; Pred. No. 1.8e-26;  
Matches 203; Conservative 0; Mismatches 121; Indels 0; Gaps 0;

QY 84 gtaacagtcgcaatgagatccaaagtgtatcgtctctagaagaagaaga 143  
DB 17 GTTTCGCAACATGAGATACCAAGATTCTCTCTCGCCGTAAAGAGAA 76  
QY 144 gtaacttcaagacacatctctgtacgaacatactatgagtcgacctgtccaa 203  
DB 77 GCCCATTTCACTGCTCATCAAGGCTTCGACGGGTGTGATGACGACCCCTTTCATCT 136  
QY 204 gaactagcgaataacagcgtctcttcttactcttgcgaagaagaagaatc 263  
DB 137 GAGTTACGTACCAAGTACAGATCTATCCGGGAGAAAGAGATGAGATTCAA 196  
QY 264 atagtcgagagcttcaaggtgagagaagaagaatgttacaacgtgttactgaaga 323  
DB 197 GTAGTAGAGAGACCTACCAAGGCCCGTGAAGAAAGTTATGCAAGTGTACCGTAAGAAA 256  
QY 324 taccgatacatatcgaagagtgacgaagaagaagaagaagaagaaga 383  
DB 257 TGGGTGATTTCACATGAGCTATACCTAGAGAGAGTTAATGATCTACTTAATGTT 316  
QY 384 ggaatacatcctcaatgttgt 407  
DB 317 GGTATTAATCCATCTAAGGTTGTT 340

## RESULT 6

BE924162 487 bp mRNA EST 02-OCT-2000  
LOCUS BE924162 487 bp mRNA EST 02-OCT-2000  
DEFINITION EST427931 potato leaves and petioles Solanum tuberosum cDNA clone  
ACCESSION BE924162  
VERSION BE924162  
KEYWORDS EST. GI:10450238  
SOURCE potato.  
ORGANISM Solanum tuberosum  
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;

## REFERENCE

Asteridae; euasterids I; Solanales; Solanaceae; Solanum. 1 (bases 1 to 487)  
van der Hoeven, R.S., Bezzerides, J., Holt, I.E., Liang, F., Cho, J., Utterback, T., Hansen, C.L., Doan, B., Bougri, O., Buell, C.R., Ronning, C.M., Fry, W.E., Tanksley, S.D. and Baker, B.  
Generation of ESTs from potato leaves and petioles  
Unpublished (2000)

## TITLE

Journal  
Contact: Cathy Ronning  
The Institute for Genomic Research  
For clone request: please contact Research Genetics, Libraries  
Division tel 1-800-711-6195, email cdna@esgen.com.

## COMMENT

## FEATURES

source  
Location/Qualifiers  
1. 487  
/organism="Solanum tuberosum"  
/cultivar="Kennebec"  
/db\_xref="taxon:4113"  
/clone="GSTB28P13"  
/clone\_1lb="potato leaves and petioles"  
/tissue\_type="leaflets and petioles"  
/dev\_stage="8 weeks old plants"  
/lab\_host="SOLR"  
/note="Vector: pBluescript SK(-); Site\_1: EcoRI; Site\_2: XhoI. Tissue was supplied by Dr. Fry (Cornell University). Leaflets and petioles were isolated from 8 week old greenhouse grown plants. The plants were watered and fertilized freely. The tissue was immediately frozen in liquid nitrogen."  
BASE COUNT 144 a 92 c 122 g 129 t  
ORIGIN

Query Match 32.0%; Score 130.4; DB 11; Length 487;  
Best Local Similarity 62.7%; Pred. No. 1.8e-26;  
Matches 203; Conservative 0; Mismatches 121; Indels 0; Gaps 0;

QY 84 gtaacagtcgcaatgagatccaaagtgtatcgtctctagaagaagaaga 143  
DB 17 GTTTCGCAACATGAGATACCAAGATTCTCTCTCGCCGTAAAGAGAA 76  
QY 144 gtaacttcaagacacatctctgtacgaacatactatgagtcgacctgtccaa 203  
DB 77 GCCCATTTCACTGCTCATCAAGGCTTCGACGGGTGTGATGACGACCCCTTTCATCT 136  
QY 204 gaactagcgaataacagcgtctcttcttactcttgcgaagaagaagaatc 263  
DB 137 GAGTTACGTACCAAGTACAGATCTATCCGGGAGAAAGAGATGAGATTCAA 196  
QY 264 atagtcgagagcttcaaggtgagagaagaagaatgttacaacgtgttactgaaga 323  
DB 197 GTAGTAGAGAGACCTACCAAGGCCCGTGAAGAAAGTTATGCAAGTGTACCGTAAGAAA 256  
QY 324 taccgatacatatcgaagagtgacgaagaagaagaagaagaagaagaaga 383  
DB 257 TGGGTGATTTCACATGAGCTATACCTAGAGAGAGTTAATGATCTACTTAATGTT 316  
QY 384 ggaatacatcctcaatgttgt 407  
DB 317 GGTATTAATCCATCTAAGGTTGTT 340

## RESULT 7

B1178667 612 bp mRNA EST 09-JUL-2001  
LOCUS B1178667 612 bp mRNA EST 09-JUL-2001  
DEFINITION EST519612 cSTE Solanum tuberosum cDNA clone cSTE15B9 5' sequence,  
ACCESSION B1178667  
VERSION B1178667  
KEYWORDS EST. GI:14644478  
SOURCE potato.  
ORGANISM Solanum tuberosum  
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Asteridae; euasterids I; Solanales; Solanaceae; Solanum.

REFERENCE 1 (bases 1 to 612)  
 AUTHORS van der Hoeven, R., Bezzerides, J., Bachem, C., Visser, R., Cho, J.,  
 Chieningo, A., Bougri, O., Buell, C.R., Roming, C., Tanksley, S. and  
 Baker, B.  
 TITLE Generation of ESTs from in vitro grown microtubers  
 JOURNAL Unpublished (2001)  
 COMMENT Contact: Cathy Roming  
 The Institute for Genomic Research  
 For clone info: please contact Research Genetics, Libraries  
 Division tel 1-800-711-6195, email cdnaesgen.com  
 Seq primer: M13P-R.  
 FEATURES  
 source  
 Location/Qualifiers  
 1..612  
 /organism="Solanum tuberosum"  
 /cultivar="Bintje"  
 /db\_xref="taxon:4113"  
 /clone\_lib="cSTE"  
 /clone\_lib="cSTE"  
 /tissue\_type="axillary buds of stem explants; growing  
 sink-tubers"  
 /dev\_stage="7, 8 and 10 days"  
 /lab\_host="SOLR"  
 /note="Vector: pBluescript SK(-); Site\_1: EcoRI; Site\_2:  
 XhoI; Tissue supplied by Christian Bachem and Richard  
 Visser (Department of Plant Breeding, Wageningen  
 University, The Netherlands). The cSTa libraries will  
 attempt to capture the induction and initiation/initial  
 growth of the tuber in an in vitro system as described in  
 Bachem et al. (Plant Journal, 1996). Small microtubers  
 develop from axillary buds attached to stem explants when  
 placed on a high sucrose medium (10%). Visible  
 morphological changes occur synchronously at day five in  
 the axillary buds. The first library, cSTa (1-20) consists  
 of axillary buds harvested on days 1-3. This targets  
 those genes involved in induction of the microtubers. The  
 following libraries, cSTa (21-40) and cSTa (41-60),  
 capture genes involved in tuber initiation and outgrowth.  
 This library is noted as p3 in Tanksley lab notebooks."  
 BASE COUNT 171 a 101 c 152 g 188 t  
 ORIGIN

Query Match 32.0%; Score 130.4; DB 11; Length 612;  
 Best Local Similarity 62.7%; Pred. No. 1.9e-26;  
 Matches 203; Conservative 0; Mismatches 121; Indels 0; Gaps 0;

84 gtatcagtcgcatgaattccaaagtgtatcgtctagaagaacagagga 143  
 ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||  
 17 GTTGTGCAACATGATACATCCAGAGATTCTCTCTCGCGTAAGAGCAAG 76  
 ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||  
 144 gcatccttcaagcaccattctgtacgacgaatactatcagtgacccctgtccaag 203  
 ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||  
 77 GCCCATTTTCACTGCTCCATCAAGCGTTCGACGGGTGTGAGAGCGACCCCTTTCATCT 136  
 ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||  
 204 gaactacgtagaataaagcttcgtcttactatctgaagaagaagacgaatc 263  
 ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||  
 137 GAGTTTACCTACCAAGTAAACGTCAGATCTATCCCGGTGAAGAAAAGAGATGAAGTTCAA 196  
 ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||  
 264 atagtctcgagagcttcaaggtgagagaagaagttaacaagtggttactcgaagaaa 323  
 ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||  
 197 GTAGTAAGAGAGACCTACCAAGGCGCGTAAGAAATTTATGCAAGTGTACCGTAAGAAA 256  
 ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||  
 324 tatcgagatacatcgagaggtgacagagaaaacgaatggaatgactgtaacctgtg 383  
 ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||  
 257 TGGGTGATTTCACATTGACCGGTATTAAGAGAAAGTTATGATGACTGTTAATGTT 316  
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 384 ggaatcacatcatatgttgtt 407  
 ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||  
 Db 317 GGTATTATTCATCTTAAGGTTGTT 340

LOCUS A1164427 340 bp mRNA EST 03-DEC-1998  
 DEFINITION A061P34U Hybrid aspen plasmid library Populus tremula x Populus  
 tremuloides cDNA 5', mRNA sequence.  
 ACCESSION A1164427  
 VERSION A1164427  
 KEYWORDS GI:3855712  
 SOURCE EST  
 ORGANISM Populus tremula x Populus tremuloides.  
 Populus tremula x Populus tremuloides  
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
 Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;  
 Rosidae; eurosids I; Malpighiales; Salicaceae; Populus.  
 1 (bases 1 to 340)  
 Sterky, F., Regan, S., Karlsson, J., Hertberg, M., Rohde, A., Holmberg  
 'A., Amin, B., Bhalerao, R., Larsson, M., Villarroel, R., Van Montagu  
 'M., Sandberg, G., Olsson, O., Teeri, T.T., Boerjan, W., Gustafsson, P.,  
 Uhlen, M., Sundberg, B. and Lundberg, J.  
 Gene discovery in the wood-forming tissues of poplar: Analysis of  
 5,692 expressed sequence tags  
 Proc. Natl. Acad. Sci. U.S.A. 95 (22), 13330-13335 (1998)  
 99007314  
 COMMENT Contact: Sterky F  
 Department of Biotechnology  
 Royal Institute of Technology (KTH)  
 Teknikringen 34, S-100 44 STOCKHOLM, Sweden  
 Tel: +46 8 790 8287  
 Fax: +46 8 24 54 52  
 Email: fredrik@biochem.kth.se  
 PCR Primers  
 FORWARD: AAGGGGATGCTGTCGACGGCG  
 BACKWARD: GCGTCGGCTCGTCAATGCG  
 Seq primer: CGTTGTAACGACGGCCAG  
 High quality sequence stop: 340.  
 Location/Qualifiers  
 1..340  
 /organism="Populus tremula x Populus tremuloides"  
 /db\_xref="taxon:47664"  
 /clone\_lib="Hybrid aspen plasmid library"  
 /tissue\_type="Cambial region"  
 /dev\_stage="1.5 m actively growing tree"  
 /lab\_host="E.coli"  
 /note="Vector: pBluescript SK; Site\_1: SalI; Site\_2: NotI;  
 Cambial region tissues, including developing xylem, the  
 meristematic cambial zone and the developing and mature  
 phloem, was harvested from 1.5 m actively growing trees.  
 cDNA was prepared and cloned into Lambda gt10a. DNA was  
 isolated and subcloned into pBluescript SK using SalI and  
 NotI restriction enzymes."  
 BASE COUNT 98 a 82 c 88 g 72 t  
 ORIGIN

Query Match 31.6%; Score 129; DB 10; Length 340;  
 Best Local Similarity 65.0%; Pred. No. 4.2e-26;  
 Matches 206; Conservative 0; Mismatches 110; Indels 1; Gaps 1;

92 cgcatagaattatccaaggtgtatcgtctgtatgaagaagcagaagaacatactt 151  
 ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||  
 Db 2 CACGATGAATTAACACCCAGAGATCTCTCTCCCGGAAACCGTAAGGCCCACTT 61  
 ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||  
 152 tcaagaccattctctgtacgacgaatactatcgaatgacacctgtccaagaactt 211  
 ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||  
 Db 62 CTCGGCGCATCTCTCGTGCTGTATCTCATGACGACCACTTCCACGACCTCCG 121  
 ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||  
 212 taagaaatacagcgttcgtcttactatctcgaagaagaagcgaatcatatgttcg 271  
 ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||  
 Db 122 TCAGAAATACACAGTGATGATCCATCCGAAAGAGATGAATGATCAAGTTGTTG 181  
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 272 cggagcttcaaggtgagagaagaagttaacaagtggttatcgaagaataatcgat 331  
 ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||  
 Db 182 TGGGACATACCAAGGAAAGGAGAGGTGTCTCAAGGTTTAAAGGAGAAATGGGAT 241  
 ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||  
 332 acatatcgagagtgaccagagaagaagcgaatggaatgactgactgtggagataca 391  
 ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

RESULT 8  
 A1164427

DB	Accession	Source	Length	Score	DB	Length	Score
Db	242 TCATGTCGACAGCATTTCAAGGCAAAAGGTTAATGATCCACTGCTTAAC	GTGGAAATTTAA	300				
Qy	392 tccatcaatgltgta	408					
Db	301 CCCTTCGAAGGTGGTGA	317					
RESULT	9						
BP517187							
LOCUS							
DEFINITION	NSI_011.D12_F NSI (nsf xylem side wood inclined) Pinus taeda CDNA clone NSI_011.D12 5', mRNA sequence.						
ACCESSION	BP517187						
VERSION	BP517187.1	GI:11604790					
KEYWORDS	EST.						
ORGANISM	loblolly pine.						
REFERENCE	Pinus taeda						
AUTHORS	Eukaryota: Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Coniferopsida; Coniferales; Pinaceae; Pinus; Pinus.						
TITLE	1 (bases 1 to 467)						
JOURNAL	Sederoff, R.						
COMMENT	Molecular Basis of Wood Formation in the Pine Megagenome Unpublished (2000)						
	Contact: Johnson, Arthur						
	North Carolina State University						
	Tel: 919 515 7800						
	Fax: 919 515 7801						
	Email: ajohnson@unc.edu						
	Seq primer: T3.						
FEATURES							
source	Location/Qualifiers						
	1..467						
	/organism="Pinus taeda"						
	/strain="Coastal plain loblolly pine from North Carolina"						
	/db_xref="taxon:3352"						
	/clone="NSI_011.D12"						
	/clone.lib="NSI (nsf xylem side wood inclined)"						
	/tissue_type="xylem"						
	/tissue="side"						
	/cell_type="side"						
	/dev_stage="juvenile"						
	/lab_host="X11-Blue"						
	/note="Vector: Bluescript SK; site_1: Eco RI; site_2: XhoI"						
	: The library is from early (spring) wood, taken from three six-year old trees (three different genotypes), in the juvenile phase. These trees were induced to form side wood by bending to a 45 degree angle and tying them to the ground. Differentiating xylem was harvested from the sides of the inclined stems, and a mixture of all three genotypes was used for the library. Oligo-dT primed cDNA was directionally cloned into the EcoRI-XhoI Bluescript SK vector arms. NOTE: The sequences contain a 'cDNA adapter' between the EcoRI site and the start of the EST. The adapter sequence is 'AATTCGCGACGAC'."						
BASE COUNT	140 a	78 c	121 g	111 t	17 others		
ORIGIN							
Query Match		31.6%	Score 129;	DB 11;	Length 467;		
Best Local Similarity		62.4%	Pred. No. 4.5e-26;				
Matches 201; Conservative		0;	Mismatches 121;	Indels	0;	Gaps	0;
Db	86 atcagtcgcatagaaglatccaaggtgtatcgtctcgtctagaagaagcagaagaagc	145					
Qy	11 111 11111111	11111111111111111111					
Db	22 AACCTTCGATATGAAGTCAATCCAGAGACAGTAGCTAGAGAGAAAGCGGGAAGC	81					
Qy	146 atacttccaagccacatctctbtagagcaaatcactcagagtgacccctgtccaagga	205					
Db	82 ACAATTACTGCCCATCTAGTGTCCGGCTATTGATGAGTGCCTTCCTTCTCTGA	141					
Qy	206 actacgtacgaataaataacgcgtctgcttcttaccattctcgaaagaagacgaagatcaat	265					
Db	142 TCGAGGACAAAGATATTAATGTTCTCTATCCCAATTAGAAAGATGATGAAGTTCAGGT	201					
Qy	266 agtgcgcgagcttccaaggtatagagaagaagaagttacacagctgttatcgaagaagaata	325					

Db	202	TGTCGGAGGAACGCTTCAAGGAGAAGCGGCCAACGGTTTCAGATTATCGTAAGAAGTG	261
Oy	326	tggatcacatatcgaggaagtgcacgagaagaagcgaatggaactgtacctgtg99	385
Db	262	GCTCATCCATGTTCGAGGCATTTACTCGGAGAAAGTCATATGTRCACACTGTGATGTGG	321
Oy	386	aatacatccatctaattgttct 407	
Db	322	TGTTACCACCATCGAANGMTGTT 343	
RESULT	10		
LOCUS	AII64301		
DEFINITION	A058p78u Hybrid aspen plasmid library	EST	03-DEC-1998
VERSION	tremuloideis cDNA 5', mRNA sequence.		
KEYWORDS	AII64301		
SOURCE	AII64301.1 GI:3855586		
ORGANISM	EST.		
REFERENCE	Populus tremula x Populus tremuloideis.		
AUTHORS	Populus tremula x Populus tremuloideis. Eukaryota; Viridiplantae; Streptophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae; eucosids I; Malpighiales; Salicaceae; Populus.		
TITLE	1 (bases 1 to 477)		
JOURNAL MEDLINE COMMENT	Steery,F., Regan,S., Karlsson,J., Hertzberg,M., Rohde,A., Holmberg ,A., Arnulf,B., Bhalerao,R., Larsson,M., Villarroel,R., Van Montagu ,M., Sandberg,G., Olsson,O., Teell,T.T., Boerjan,W., Gustafsson,P., Uhlen,M., Sundberg,B. and Lundberg,J. Gene discovery in the wood-forming tissues of poplar: Analysis of 5,692 expressed sequence tags Proc. Natl. Acad. Sci. U.S.A. 95 (22), 13330-13335 (1998) 99007314 Contact: Steery F Department of Biotechnology Royal Institute of Technology (KTH) Teknikringen 34, S-100 44 STOCKHOLM, Sweden Tel.: +46 8 790 8287 Fax: +46 8 24 54 52 Email: fredrik@biochem.kth.se PCR primers FORWARD: AAAGGGGATGCTGCTCGAAGCG BACKWARD: GCTTCGGCTGCTGATGTGTGTG Seq primer: CGTGTAAACGACGCGCAG High quality sequence stop: 477. Location/Qualifiers 1..477 /organism="Populus tremula x Populus tremuloideis" /db_xref="taxon:47664" /clone_lib="Hybrid aspen plasmid library" /tissue_type="Cambial region" /dev_stage="1.5 m actively growing tree" /lab_note="E.coli" /note="Vector: pBluescript SK; Site_1: SalI; Site_2: NotI Cambial region tissues, including developing xylem, the meristematic cambial zone and the developing and mature phloem, was harvested from 1.5 m actively growing trees. cDNA was prepared and cloned into Lambda gt2a. DNA was isolated and subcloned into pBluescript SK using SalI and NotI restriction enzymes."		
BASE COUNT	130 a 107 c 130 g 107 t	3 others	
ORIGIN			
Query Match	31.6%; Score 128.8; DB 10;	Length 477;	
Best Local Similarity	62.8%; Pred. No. 5.1e-26;		
Matches 199; Conservative	0; Mismatches 118; Indels	0; Gaps	0
Oy	92	cgcacatgaagtattccaagtgtgatcgttcgtatagaagaacagagaacacatca 151	
Db	8	CACAAATGAAGNACAACCCAGAGAGTCTCTCTCCGCCCGGAGAAACCGTAAGGCCACACTT 67	

RESULT	11
AM289566	
LOCUS	
DEFINITION	AM289566 471 bp mRNA
ACCESSION	NNV002G02F Nsf xylem Normal wood Vertical Pinus taeda cDNA clone
VERSION	AM289566 5', mRNA sequence.
KEYWORDS	AM289566.1 GI:6696202
SOURCE	EST.
ORGANISM	loblolly pine.
	Pinus taeda
	16-JAN-2000

REFERENCE	
AUTHORS	Sederoff, R.
TITLE	Molecular Basis of Wood Formation in the Pine Megagenome
JOURNAL	Unpublished (2000)
COMMENT	Contact: Johnson, Arthur

North Carolinastate University  
Tel: 919 515 7800  
Fax: 919 515 7801  
Email: [ajohnson@unity.ncsu.edu](mailto:ajohnson@unity.ncsu.edu)  
Seq primer: T3.

FEATURES	Location/Qualifiers
source	1. .471

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/organism="Pinus taeda"
/db_xref="taxon:3352"
/clone="NXNV002G02"
/clone_lib="Nsf Xylem Normal wood Vertical"
/note="Vector: Bluescript SK; Site 1: Eco RI; The
sequences contain a 'cDNA adapter' between the EcoRI site
and the start of the EST. The adapter sequence is
'AATCGGCGACGAG.'"

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Query Match	31.5%;	Score 128.4;	DB 10;	Length 471
Best Local Similarity	62.4%;	Pred NO	5.6e-26;	

Matches	201;	Conservative	0;	Mismatches	121;	Indels	0;	Gaps	0;
---------	------	--------------	----	------------	------	--------	----	------	----

OY 86 atcagtcgcacatgaagtattccaaagttgtatcgtctctaagaagaagcagagaagaac 145  
| | | | |  
Dd 55 AACCTTCATATGAAGTACATCCACAGAGTCAGTCAGTCCTTAGGAGAAAGACCGGAAGGC 114  
| | | | |

QY 146 atacttcaagcaccatcttctgtacgacgataactatcatgagtgcaccctgtccaagga 205

Db 115 ACATTTTACTGCCCATCTAGTGTCCGGCGATTTTGTAGTGTCCGCTTTCTCTGA 174

Oy 206 actacgtacgcaatatcacagcgttctgtcttctaactattcgaaaagaacgaatcat 265

Db 175 TCTGAGGACACAGTAAATGTTCTTCTATCCCAATTAGAAGCATGATCAAGTTCAGGT 234

QY 266 agtccgagagcttcaagggtgagagaagaaagttacacgtyttatcgaanaa 325  
Db 235 TATGGAGGAACGTTTCAAGGAGGAGGCGCAAGTTGTTCAAGTTATCGTAAGACTG 294  
QY 326 tcgatacatatcgagagagtgaccgagaaaaagaaagaaatgaatgaactctgtgg 385  
Db 235 GGTATTCATCTGTAGGCGCACTACTCGGGGAAAGTCATGTGTACAACTGTGAATGTTGG 354  
QY 386 aatacatcatcatatgttt 407  
Db 355 TGTTCACCCATCGAAGTGT 376

RESULT	12
AL388757	
LOCUS	AL388757
DEFINITION	AL388757 389 bp mRNA
VERSION	MBSC0E10F1
ACCESSION	MBSC Medicago truncatula cDNA clone MTEC50E10 T3, mRNA
KEYWORDS	sequence.
SOURCE	AL388757.1 GI:9688508
	EST.
	barrel medic.

ORGANISM	REFERENCE AUTHORS	TITLE JOURNAL	COMMENT
Medicago truncatula	Journel,E.P., Crespeau,H., Van-Tuinen,D., Gouzy,J., Tallion,O., Niebel,A., Carreau,V., Chataigner,O., Kahn,D., Gianinazzi-Pearson,V. and Gamas,P.	Medicago truncatula ESTs from endomycorrhizal roots Unpublished (2000)	Contact: Genoscope
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae; eurosids I; Fabales; Fabaceae; Papilionoideae; Trifolieae Medicago.	1 (bases 1 to 389) Journel,E.P., Crespeau,H., Van-Tuinen,D., Gouzy,J., Tallion,O., Niebel,A., Carreau,V., Chataigner,O., Kahn,D., Gianinazzi-Pearson,V. and Gamas,P.	Medicago truncatula ESTs from endomycorrhizal roots Unpublished (2000)	Contact: Genoscope

Genoscope - Centre National de Séquençage  
BP 191 91006 Evry cedex - France  
Email: [seqref@genoscope.cns.fr](mailto:seqref@genoscope.cns.fr), Web : [www.genoscope.cns.fr](http://www.genoscope.cns.fr)  
Contact : Pascal Gamas and Etienne-Pascal Journet, Laboratoire de  
Biologie Moléculaire des Relations Plantes-Microorganismes,  
CNRS-INRA, BP 27 31326 Castanet-Tolosan Cedex, France (Email :  
[M-est@toulouse.inra.fr](mailto:M-est@toulouse.inra.fr) Website :  
<http://sequence.toulouse.inra.fr/Mtuncatula.html>).

FEATURES	Location/Qualifiers
source	1. .389

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"organism="Medicago truncatula"
"cultivar="Jemalong"
"db_xref="taxon:3880"
"clone="MtBC5OE10"
"clone_lib="MtBC"
"tissue_type="arbuscular mycorrhiza"
"dev_stage="harvested 3 weeks post inoculation with Glomus
intraradices"

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Notes: "Vector: pBluescript SK<sup>+</sup>; Site\_1: EcoRI; Site\_2: XhoI; M. truncatula sterilised seeds were germinated for 72h at 25 °C, before transplanting into a 1/3 Epilobes soil : 2/3 calcined terragreen mix in the presence of onion root fragments colonized by the arbuscular mycorrhizal fungus Glomus intraradices (Scherck & Smith, isolate IP48 ). The plants were watered every day and twice a week with a modified nutrient long Ashton solution without phosphate but with a high level of nitrate. After 3 weeks RNA was extracted from whole root systems. cDNA was prepared from polyA<sup>+</sup> enriched RNA. The cDNA was directionally ligated into Uni-Tap XR vector from Stratagene and packaged using GigaPack gold packaging extracts. Plasmids containing cDNA inserts were mass-excised from phage stocks using ExaSart helper phage and propagated in SOLR cells. Clone ordering and sequencing was performed by the Centre National de Séquençage (Genoscope, Evry, France). Note : EST may be of *U. lutea* origin."

BASE COUNT	129 a	70 c	88 g	102 t
ORIGIN	.	.	.	.





FEATURES	Location/Qualifiers
source	1. 525
	/organism="Lycopersicon esculentum"
	/cultivar="TA496"
	/db_xref="taxon:4081"
	/clone="CLEB3G6"
	/clone_1ib="tomato shoot, Cornell"
	/tissue_type="shoot meristem"
	/dev_stage="8 week old plants"
	/lab_host="XLOL"
	/note="Vector: PBK_CMV, Site_1: EcoRI, site_2: XhoI; cLEB3G6 - Tomato Shoot Meristem EST library. Oligo-dT primed cDNA library made from tomato vegetative shoots including meristems and small expanding leaves."
BASE COUNT	153 a 104 c 135 g 133 t
ORIGIN	
Query Match	31.0%; Score 126.4; DB 10; Length 525;
Best Local Similarity	62.8%; Pred. No. 2.5e-25;
Matches 196;	Conservative 0; Mismatches 116; Indels 0; Gaps 0
QY	96 atgaagatctccaaagcttgcgttcgtctagagaagaacagaggaagaaagcatttcaa 155
DB	18 ATGAAGTACCAATCCACAGAGTATCCTCTCCGCCGGAAGACGAGAGGCTCATTTACG 77
QY	156 gcaccattctctgacgaacatccatcagatgacacccctgtccaagaactacgtaac 215
DB	78 GCGCCTTCAGTGGCGCCGGATTTTAATGACGCGACCCCTTATGCTCCGAGTTACGTGA 137
QY	216 aatacagcgttcgttccttaccatttcgaaaaagaacgaagtaatacatagtcgcgga 275
DB	138 AAGTACACGTAAAGTATGATCCGCGGAGAGAAAGATGACGAAGTTCAAGTTGCTGGA 197
QY	276 gcttcaagsgttagagaagaagaagttacaacgctgttcgaagaagaatcgcatacat 335
DB	198 ACTTACAAGGCGCGTGAACGGGAAGTTGTTCAAGGTACCGTACGAATGGGTATCCAC 257
QY	336 atcgaagagatgacccagagaagaacgaatggaatgcatgtaacctgtggaataatcaca 395
DB	258 ATTGAACGTGTATACACGAGAGAGCATGATGATCTGTAAGCGTTGATTCATCCT 317
QY	396 tctaattgtt 407
DB	318 TCGAAGTGTCT 329
RESULT 15	
LOCUS	A1772648
DEFINITION	EST253748 tomato resistant, Cornell Lycopersicon esculentum cDNA clone CLEB3G6, mRNA sequence.
ACCESSION	A1772648
VERSION	A1772648.1 GI:5270689
KEYWORDS	EST.
SOURCE	tomato.
ORGANISM	Lycopersicon esculentum
REFERENCE	Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Asteridae; euasterids I; Solanales; Solanaceae; Solanum;
AUTHORS	Lycopersicon.
	1 (bases 1 to 527)
	D' Ascenzo, M., He, X., Lyman, J., Matero, A. L., Vision, T., Holt, I. E., Liang, F., Upton, J., Ronning, C. M., Craven, M. B., Fujii, C. Y., Bowman, C. L., Nieman, W., Fraser, C. M., Venter, J. C., Tanksley, S. D., Giovannoni, J. J., and Matlin, G. B.
	Generation of ESTs from Pseudomonas resistant tomato
	Unpublished (1999)
TITLE	Contact: CUGI
JOURNAL	Clemson University Genomics Institute
COMMENT	Clemson University
	100 Jordan Hall, Clemson, SC 29634, USA
	Email: <a href="http://www.genome.clemson.edu/orders/index.html">http://www.genome.clemson.edu/orders/index.html</a>

```

FEATURES
5 prime sequence.
Location/Qualifiers
1. 527
/organism="Lycopersicon esculentum"
/cultivar="R11-12 (35S)::pTo in Rio Grande x Money Maker)"
/db_xref="taxon:4081"
/clone="CLER3M12"
/clone_1lb="tomato resistant, Cornell"
/tissue_type="leaf"
/dev_stage="4-week old"
/lab_host="SOLR"
/note="vector: pBluescript SK(-); Site_1: EcoRI; Site_2:
XhoI; cDER - Tomato Pseudomonas Resistant EST library.
directionally cloned. cDNAs inserted into pBluescript SK(-)
at 5' end with EcoRI and 3' end with XhoI site."
BASE COUNT 155 a 104 c 133 g 135 t
ORIGIN

Query Match 31.0%; Score 126.4; DB 10; Length 527;
Best Local Similarity 62.8%; Pred. No. 2,5e-25;
Matches 196; Conservative 0; Mismatches 116; Indels 0; Gaps 0;

QY 96 atgaagattccaagttgatacgtcgtctagaaagaacagaggaacatacttcaa 155
||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 15 ATGAAGTACAAATCCAAAGATATCTCTCTCTCGCGGAAGACGAGAAAGCCTATTTCACG 74

QY 156 gacacatctctgtacgaacgaatcactcatgagtgacccttggtccaagaactaagtcag 215
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Db 75 GCGCCTTCAAGTGC CGCGCGCGGATTTTAATGAGCGGACCCCTTATCGTCCGAGTTACGTGTGA 134

QY 216 aaatacagcgttcgtcttacciatlccgaaaagaacgaaglaatacatagttccgga 275
||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 135 AAGTACAAACGTAAAGATCTATCGCGGTGAGGAAGATGACGAAGTTCCAGGTGTTGCTGGA 194

QY 276 gcttccaaggttagaagaagaagttlcaaacgtgttatacgaagaataatcogatacat 335
||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 195 ACTTACAAAGGCGGTGACGGGAAAGTTGTCCAAAGTGTACCCGTAAAGAAATGGGTATCCAC 254

QY 336 atcgagagagtgaccagaaagaacgaatggaatgactgtaccgtgtggaatacatcca 395
||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 255 ATTGAACGTATTAACACAGAGAGAGAGAGTCAATGATCTACTGTGAACGTTGGTATTCATCT 314

QY 396 tctaatgttgtt 407
||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 315 TCGAAGGTGTT 326

Search completed: March 2, 2002, 20:28:49
Job time: 1519 sec

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MON Mar 4 11:24:44 2002

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